

#1



	1		50
EG327	MNKIYRIIWN SALNAWVAWS ELTRNHTKRA SATVATAVLA TLLFATVQAS.		
BZ198	MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN		
BZ10	MNKISRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN		
H15	MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN		
EG329	MNEILRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS		
PMC21	MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS		
H38	MNKIYRIIWN SALNAWVAWS ELTRNHTKRA SATVKTAVLA TLLFATVQAN		
P20	MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLSATVQAN		
Z2491	MNKIYRIIWN SALNAWVAWS ELTRNHTKRA SATVKTAVLA TLLFATVQAN		
H41	MNKIYRIIWN SALNAWVAWS ELTRNHTKRA SATVKTAVLA TLLFATVQAN		
Consensus	<u>MN-I-RIWN SALNAWV-VS ELTRNHTKRA SATV-TAVLA TLL-ATVQA-</u>		

C1

	51		100
EG327	TTDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.VTED SNWGJVYFDKK		
BZ198	ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK		
BZ10	ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK		
H15	ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK		
EG329	ANNEEQEEDL YLDPLRLRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK		
PMC21	ANNEEQEEDL YLDPLQRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK		
H38	ATDED..EEE ELEPVVRSL VLQFMIDKEG NGENE.STGN IGWSIYYDNH		
P20	ATDTD..EDE ELESVARSL VLQFMIDKEG NGEIESTGDI GWSIYYDDHN		
Z2491	ATDED..EEE ELESVQR.SV VGSIQASMEG SGELET...I SLSMTNDSKE		
H41	ATDED..EEE ELESVQR.SV VGSIQASMEG SVELET...I SLSMTNDSKE		
Consensus	<u>----- -L--V-R--- V-----EG --E-E-----</u>		

V1

	101		150
EG327	GVLTAGTITL KAGDNLKIKQ NTNENTNASSFTYSLK KDLTDLTSVG		
BZ198	RVLKAGAITL KAGDNLKIKQ NTNENTNDSSFTYSLK KDLTDLTSVE		
BZ10	RVLKAGAITL KAGDNLKIKQ NTNENTNENT NDSSFTYSLK KDLTDLTSVE		
H15	RVLKAGAITL KAGDNLKIKQ NTNENTNENT NDSSFTYSLK KDLTDLTSVE		
EG329	GVLTAREITL KAGDNLKIKQ NG...TN...FTYSLK KDLTDLTSVG		
PMC21	GVLTAREITL KAGDNLKIKQ NG...TN...FTYSLK KDLTDLTSVG		
H38	NTLHGATVTL KAGDNLKIKQ NTNKNENT NDSSFTYSLK KDLTDLTSVE		
P20	TLHG.ATVTL KAGDNLKIKQ SGKD.....FTYSLK KELKDLTSVE		
Z2491	FVDPYIVVTL KAGDNLKIKQ NTNENTNASSFTYSLK KDLTGLINVE		
H41	FVDPYIVVTL KAGDNLKIKQ NTNENTNASSFTYSLK KDLTGLINVE		
Consensus	<u>-----TL KAGDNLKIKQ ----- -----FTYSLK K-L--L--V-</u>		

V1

C2

V2

C3

FIG. 1

	151		200		
EG327	TEKLSFSANS	NKVNITSDETK	GLNFAKKTAE	TNGDTTVHLN	GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDETK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDETK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDETK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDETK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDETK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDETK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDETK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIIISDETK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDTL
H41	TEKLSFGANG	KKVNIIISDETK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDML
Consensus	<u>TEKLSF-AN-</u>	<u>-KVNI-SDTK</u>	<u>GLNFAK-TA-</u>	<u>TNGD-TVHLN</u>	<u>GIGSTLTD-L</u>

C3

	201		250		
EG327	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS.. DNV
BZ198	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS.. DNV
BZ10	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS.. DNV
H15	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS.. DNV
EG329	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS.. DNV
PMC21	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS.. DNV
H38	LNTGATTNVT	NDNVTDDKKK	RAASVKDVLN	AGWNIKGVP	GTTAS.. DNV
P20	AGSSASHVDA	GNQST.. HYT	RAASIKDVLN	AGWNIKGVK	GSTTGQSENV
Z2491	AGSSASHVDA	GNQST.. HYT	RAASIKDVLN	AGWNIKGVK	GSTTGQSENV
H41	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS.. DNV
Consensus	<u>-----A-----</u>	<u>-----T-----</u>	<u>RAAS-KDVLN</u>	<u>AGWNIKGVK-</u>	<u>G-T-----NV</u>

V3

C4

V4

	251		300		
EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
H38	DFVHTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
Consensus	<u>DFV-TYDTVE</u>	<u>FLSADTKTTT</u>	<u>VNVESKDNGK</u>	<u>-TEVKIGAKT</u>	<u>SVIKEKDGL</u>

C5

FIG. 1

	301	350
EG327	VTGKDKGEND SSTDKGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
BZ198	VTGKGKDENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
BZ10	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
H15	VTGKGKDENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
EG329	VTGKDKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
PMC21	VTGKDKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
H38	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
P20	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
Z2491	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
H41	VTGKGKGENG SSTDEGEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	
Consensus	<u>VTGK-K-EN-</u> SSTD-GEGLV TAKEVIDAVN KAGWRMKTTT ANGQTGQADK	

C5

	351	400
EG327	FETVTSGTNV TFASGKGT TA TVSKDDQGNI TVMYDVNGD ALNVNQLQNS	
BZ198	FETVTSGTNV TFASGKGT TA TVSKDDQGNI TVKYDVNGD ALNVNQLQNS	
BZ10	FETVTSGTKV TFASGNGT TA TVSKDDQGNI TVKYDVNGD ALNVNQLQNS	
H15	FETVTSGTKV TFASGNGT TA TVSKDDQGNI TVKYDVNGD ALNVNQLQNS	
EG329	FETVTSGTNV TFASGKGT TA TVSKDDQGNI TVMYDVNGD ALNVNQLQNS	
PMC21	FETVTSGTNV TFASGKGT TA TVSKDDQGNI TVMYDVNGD ALNVNQLQNS	
H38	FETVTSGTNV TFASGKGT TA TVSKDDQGNI TVKYDVNGD ALNVNQLQNS	
P20	FETVTSGTKV TFASGNGT TA TVSKDDQGNI TVKYDVNGD ALNVNQLQNS	
Z2491	FETVTSGTNV TFASGKGT TA TVSKDDQGNI TVMYDVNGD ALNVNQLQNS	
H41	FETVTSGTKV TFASGNGT TA TVSKDDQGNI TVKYDVNGD ALNVNQLQNS	
Consensus	<u>FETVTSGT-V</u> TFASG-GT TA TVSKDDQGNI TV-YDVNGD ALNVNQLQNS	

C5

	401	450
EG327	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
BZ198	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
BZ10	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
H15	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
EG329	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
PMC21	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
H38	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
P20	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
Z2491	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EISRNGKNID	
H41	GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID	
Consensus	<u>GWNLDKAVA</u> GSSGKVISGN VSPSKGMDE TVNINAGNNI EI-RNGKNID	

C5

	451		500		
EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDTNK	PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKG	LNVGSKDANK	PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Consensus	<u>IATSM-PQFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A</u>	<u>LNVGSK--NK</u>	<u>PVRITNVAPG</u>

C5

	501		550		
EG327	VKEGDVTNVA	QLKGVAQNLN	NHIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
H15	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLAQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNLN</u>	<u>N-IDNV-GNA</u>	<u>RAGIAQAIAT</u>	<u>AGL-QAYLPG</u>

C5

	551		600		
EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ198	KSMMAIGGGDT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGASASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW	IIKGTASGNS	RGHFGASASV
Consensus	<u>KSMMAIGGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW</u>	<u>-IKGTASGNS</u>	<u>RGHFG-SASV</u>

C5

601
EG327 GYQW.
BZ198 GYQW.
BZ10 GYQW.
H15 GYQW.
EG329 GYQW.
PMC21 GYQW.
H38 GYQW.
P20 GYQW.
Z2491 GYQW.
H41 GYQW.
Consensus GYQW.
C5

FIG. 1

1 70
 H15 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
 BZ10 ATGAACAAAA TATCCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
 BZ198 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
 P20 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT AGTCGTATCC GAGCTCACAC
 H38 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
 Z2491 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
 H41 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
 EG329 ATGAACGAAA TATTGCGCAT CATTGGAAT AGCCTCA ATGCCTGGGT CGTTGTATCC GAGCTCACAC
 PMC21 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCATGGGT CGTCGTATCC GAGCTCACAC
 EG327 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
 Consensus ATGAAC-AAA TAT--CGCAT CATTGGAAT AG-GCCCTCA ATGC-TGGGT -G--GTATCC GAGCTCACAC

C1

71 140
 H15 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGGCACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 BZ10 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGGCACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 BZ198 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGGCACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 P20 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGGCACCGC CGTATTGGCG ACACTGCTGT CCGCAACGGT
 H38 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACGCTGTTGT TTGCAACGGT
 Z2491 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 H41 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 EG329 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
 PMC21 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGGCACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
 EG327 GCAACCACAC CAAACGCGCC TCCGCAACCG TG--GACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 Consensus GCAACCACAC CAAACGCGCC TCCGCAACCG TG--GACCGC CGTATTGGCG AC-CTG-TGT --GCAACGGT

C1

141 210
 H15 TCAGGCGAAT GCTACCGATG ACGAC..... GATT TA TATTAGAAC CCGTACAACG CACTGCTGTC
 BZ10 TCAGGCGAAT GCTACCGATG ACGAC..... GATT TA TATTAGAAC CCGTACAACG CACTGCTGTC
 BZ198 TCAGGCGAAT GCTACCGATG ACGAC..... GATT TA TATTAGAAC CCGTACAACG CACTGCTGTC
 P20 TCAGGCGAAT GCTACCGATA CCGAT..... GAAGATGAA GAGTTAGAAC CCGTAGCACG CTCTGCTCTG
 H38 TCAGGCGAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAC CCGTAGTACG CTCTGCTCTG
 Z2491 TCAGGCGAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAC CCGTACAACG CTCTGTCGA
 H41 TCAGGCGAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAC CCGTACAACG CTCTG...TC
 EG329 TCAGGCGAAGT GCTAACAAATG AAGAGCAAGA AGAAGATT A TATTAGACC CCGTGCTACG CACTGTTGCC
 PMC21 TCAGGCGAAGT GCTAACAAATG AAGAGCAAGA AGAAGATT A TATTAGACC CCGTGCTACG CACTGTTGCC
 EG327 TCAGGCGAAGT ACTACCGATG ACGAC..... GATT TA TATTAGAAC CCGTACAACG CACTGCTGTC
 Consensus TCAGGC-A-T -CTA-C-AT- --GA-----GA---A -A-TTAA- CCGT---ACG C-CTG-----

C1

V1

FIG. 2

	211
H15	GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
BZ10	GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
BZ198	GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
P20	GTGTTGCAAT TCATGATCGA TAAAGAAGGC AATGGAGAAA TCGAATCTAC AGGAGA...T ATAGGTTGGA
H38	GTGTTGCAAT TCATGATCGA TAAAGAAGGC AATGGAGAAA ACGAATCTAC AGGAGA...T ATAGGTTGGA
Z2491	GGG..AGCAT TCAAG.CCAG TATGGAAGGC AGCGGCGAAT TGGAACAGAT ATCAT....T ATCAATGACT
H41	GTAGGGACCA TTCAAGCCAG TATGGAAGGC AGCGTCAAT TGGAACAGAT A.....TCATTATCAA
EG329	GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAAAAGT AGAAGAAAAT TCAGATTGGG
PMC21	GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAAAAGT AGAAGAAAAT TCAGATTGGG
EG327	GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGTTAC AGAAGA...T TCAAATTGGG
Consensus	<u>G-----T-----C-- TA--GAAGGC A--G--GAA- --GAA-----A-----</u>

V1

	281
H15	CAGTATATT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCTC AAAGCCGGCG ACAACCTGAA
BZ10	CAGTATATT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCTC AAAGCCGGCG ACAACCTGAA
BZ198	CAGTATATT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCTC AAAGCCGGCG ACAACCTGAA
P20	GTATATATTA CGACGATCAC AACACTCTAC ACGGCGAAC CGTTACCCCTC AAAGCCGGCG ACAACCTGAA
H38	GTATATATTA CGACAATCAC AACACTCTAC ACGGCGAAC CGTTACCCCTC AAAGCCGGCG ACAACCTGAA
Z2491	AACGACAGCA AGGAATTGT AGACCCATAC ATAGTA.... GTTACCCCTC AAAGCCGGCG ACAACCTGAA
H41	TGACTAACGA CAGCAAGGAA TTTGTAGACC CATACTAGT AGTTACCCCTC AAAGCCGGCG ACAACCTGAA
EG329	CAGTATATT CAACGAGAAA GGAGTACTAA CAGCCAGAGA AATCACCCCTC AAAGCCGGCG ACAACCTGAA
PMC21	CAGTATATT CAACGAGAAA GGAGTACTAA CAGCCAGAGA AATCACCCCTC AAAGCCGGCG ACAACCTGAA
EG327	GAGTATATT CGACAAGAAA GGAGTACTAA CAGCCGGAAC AATCACCCCTC AAAGCCGGCG ACAACCTGAA
Consensus	<u>-----A----- -----T-ACCCCTC AAAGCCGGCG ACAACCTGAA</u>

V1

C2

	351
H15	AATCAAACAA AACACCAATG AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCCCTGAAA
BZ10	AATCAAACAA AACACCAATG AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCCCTGAAA
BZ198	AATCAAACAA AACACCAATG AAAACACC..... AATGACAGTA GCTTCACCTA CTCCCTGAAA
P20	AATCAAACAA AGCGGCAAAG A..... .CTTCACCTA CTCGCTGAAA
H38	AATCAAACAA AACACCAATA AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCGCTGAAA
Z2491	AATCAAACAA AACACCAATG AAAACACC..... AATGCCAGTA GCTTCACCTA CTCGCTGAAA
H41	AATCAAACAA AACACCAATG AAAACACC..... AATGCCAGTA GCTTCACCTA CTCGCTGAAA
EG329	AATCAAACAA AAC..... G..... GCACAA ACTTCACCTA CTCGCTGAAA
PMC21	AATCAAACAA AAC..... G..... GCACAA ACTTCACCTA CTCGCTGAAA
EG327	AATCAAACAA AACACCAATG AAAACACC..... AATGCCAGTA GCTTCACCTA CTCGCTGAAA
Consensus	<u>AATCAAACAA A-C-----CTTCACCTA CTC-CTGAAA</u>

C2

V2

C3

FIG. 2

421 490

H15 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGT AATAAAGTCA
 BZ10 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGT AATAAAGTCA
 BZ198 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGT AATAAAGTCA
 P20 AAAGAGCTGA AAGACCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGT AATAAAGTCA
 H38 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGC AATAAAGTCA
 Z2491 AAAGACCTCA CAGGCCGTGAT CAATGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGC AAGAAAGTCA
 H41 AAAGACCTCA CAGGCCGTGAT CAATGTGAA ACTGAAAAAT TATCGTTGG CGCAAACGGC AAGAAAGTCA
 EG329 AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT TATCGTTAG CGCAAACGGC AATAAAGTCA
 PMC21 AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT TATCGTTAG CGCAAACGGC AATAAAGTCA
 EG327 AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT TATCGTTAG CGCAAACAGC AATAAAGTCA
 Consensus AAAGA-CT-A -AG--CTGA- CA-TGTTG-A ACTGAAAAAT TATCGTT-G CGAACAC-G- AA-AAAGTCA

C3

491 560

H15 ACATCACAAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
 BZ10 ACATCACAAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
 BZ198 ACATCACAAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
 P20 ACATCACAAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
 H38 ACATCACAAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 Z2491 ACATCATAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 H41 ACATCATAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 EG329 ACATCACAAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 PMC21 ACATCACAAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 EG327 ACATCACAAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGAG ACCAACGGCG ACACCACGGT
 Consensus ACATCA-AAG CGACACCAAA GGCTTGAATT T-GCGAA-A AACGGCTG-G AC-AACGGCG AC-CCACGGT

C3

561 630

H15 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCCAC AAACGTAACC
 BZ10 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCCAC AAACGTAACC
 BZ198 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCCAC AAACGTAACC
 P20 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT CGGGGTTCTT CTGCTTCTCA CGTTGATGCG
 H38 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCCAC AAACGTAACC
 Z2491 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT CGGGGTTCTT CTGCTTCTCA CGTTGATGCG
 H41 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATATGCTG CTGAATACCG GAGCGACCCAC AAACGTAACC
 EG329 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCCAC AAACGTAACC
 PMC21 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCCAC AAACGTAACC
 EG327 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCCAC AAACGTAACC
 Consensus TCATCTGAAC GGTAT-GGTT CGACTTTGAC CGATA-GCT- --G-T-C- --GC-C--- ---G-C-

C3

V3

631 700

H15 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGCAA CGTTAAAGA CGTATTAAAC GCAGGCTGGA
 BZ10 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGCAA CGTTAAAGA CGTATTAAAC GCAGGCTGGA
 BZ198 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGCAA CGTTAAAGA CGTATTAAAC GCAGGCTGGA
 P20 GGTAAACAAA GTACACATTA C.....ACT CGTCAGCAA GTATTAAGGA TGTGTTGAAT GCGGGTTGGA
 H38 AACGACAACG TTACCGATGA CAAGAAAAAA CGTGGGCAA CGTTAAAGA CGTATTAAAC GCAGGCTGGA
 Z2491 GGTAAACAAA GTACACATTA C.....ACT CGTCAGCAA GTATTAAGGA TGTGTTGAAT GCGGGTTGGA
 H41 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGCAA CGTTAAAGA CGTATTAAAC GCAGGCTGGA
 EG329 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGCAA CGTTAAAGA CGTATTAAAC GCTGGCTGGA
 PMC21 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGCAA CGTTAAAGA CGTATTAAAC GCTGGCTGGA
 EG327 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGCAA CGTTAAAGA CGTATTAAAC GCAGGCTGGA
 Consensus ---AC-A-- -TAC--AT-A C-----A-- CGTGC-GCAA G--TTAA-GA -GT-TT-AA- GC-GG-TGGA

V3 C4

701 770

H15 ACATTAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA
 BZ10 ACATTAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTC GATTCGTCC GCACTTACGA
 BZ198 ACATTAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA
 P20 ATATTAAGGG TGTTAAACT GGCTCAACAA CTGGTCAATC AGAAAATGTC GATTCGTCC GCACTTACGA
 H38 ACATTAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC ACACTTACGA
 Z2491 ATATTAAGGG TGTTAAACT GGCTCAACAA CTGGTCAATC AGAAAATGTC GATTCGTCC GCACTTACGA
 H41 ACATTAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA
 EG329 ACATTAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA
 PMC21 ACATTAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA
 EG327 ACATTAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTCGTCC GCACTTACGA
 Consensus A-ATTAAGG -GTTAAACCC- GG--CAACAG- CT-----TC -GA-AA-GT- GATTCGTCC -CACTTACGA

C4 V4 C5

771 840

H15 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 BZ10 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 BZ198 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 P20 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 H38 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 Z2491 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 H41 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 EG329 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 PMC21 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 EG327 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG
 Consensus CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAGA CAACGGCAAG

C5

841 910

H15 AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 BZ10 AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 BZ198 AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 P20 AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 H38 AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 Z2491 AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 H41 AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 EG329 AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 PMC21 AAAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 EG327 AGAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATCA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 Consensus A-AAACCGAAG TTAAAATCGG TCGGAAGACT TCTGTTATCA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA

C5

FIG. 2

10/31

H15	AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	980
BZ10	AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
BZ198	AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
P20	AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
H38	AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
Z2491	AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
H41	AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
EG329	AAGACAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
PMC21	AAGACAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
EG327	AAGACAAGG CGAGAATGAT TCTTCTACAG ACAAAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	
Consensus	<u>AAG-CAAAG-</u> CGAGAATG-T TCTTCTACAG AC AAAGGCAGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA	

C5

H15	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	1050
BZ10	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
BZ198	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
P20	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
H38	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
Z2491	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
H41	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
EG329	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
PMC21	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
EG327	TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	
Consensus	<u>TGCAGTAAAC</u> AAGGCTGGTT GGAGAATGAA AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG	

C5

H15	TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	1120
BZ10	TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
BZ198	TTTGAAACCG TTACATCAGG CACAAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
P20	TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
H38	TTTGAAACCG TTACATCAGG CACAAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
Z2491	TTTGAAACCG TTACATCAGG CACAAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
H41	TTTGAAACCG TTACATCAGG CACAAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
EG329	TTTGAAACCG TTACATCAGG CACAAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
PMC21	TTTGAAACCG TTACATCAGG CACAAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
EG327	TTTGAAACCG TTACATCAGG CACAAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	
Consensus	<u>TTTGAAACCG</u> TTACATCAGG CACAAAATGTA ACCTTTGCTA GTGGTAATGG TACAAC TGCG ACTGTAAGTA	

C5

H15	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	1190
BZ10	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
BZ198	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
P20	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
H38	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
Z2491	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
H41	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
EG329	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
PMC21	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
EG327	AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	
Consensus	<u>AAGATGATCA</u> AGGCAACATC ACTGTTAAGT ATGATGAAA TGTCCGGCAT GCCCTAAACG TCAATCAGCT	

C5

FIG. 2

1191	1260
H15	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
BZ10	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
BZ198	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
P20	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
H38	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
Z2491	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
H41	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
EG329	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
PMC21	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
EG327	GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
Consensus	<u>GCAAAACAGC GGTTGGAATT TGGAATCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT</u>

C5

1261	1330
H15	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
BZ10	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
BZ198	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
P20	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H38	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Z2491	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H41	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG329	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
PMC21	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG327	GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Consensus	<u>GTTTGCAGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC</u>

C5

1331	1400
H15	GCAACGGCAA AAATATCGAC ATGCCACTT CGATGACCCC GCAATTTC GCGTTTCGC TCGGGCGGGG
BZ10	GCAACGGCAA AAATATCGAC ATGCCACTT CGATGACCCC GCAATTTC GCGTTTCGC TCGGGCGGGG
BZ198	GCAACGGTAA AAATATCGAC ATGCCACTT CGATGCGCC GCAATTTC GCGTTTCGC TCGGGCGGGG
P20	GCAACGGCAA AAATATCGAC ATGCCACTT CGATGACCCC GCAATTTC GCGTTTCGC TCGGGCGGGG
H38	GCAACGGTAA AAATATCGAC ATGCCACTT CGATGACCCC GCAATTTC GCGTTTCGC TCGGGCGGGG
Z2491	GCAACGGTAA AAATATCGAC ATGCCACTT CGATGCGCC GCAATTTC GCGTTTCGC TCGGGCGGGG
H41	GCAACGGCAA AAATATCGAC ATGCCACTT CGATGACCCC GCAATTTC GCGTTTCGC TCGGGCGGGG
EG329	GCAACGGTAA AAATATCGAC ATGCCACTT CGATGACCCC GCAATTTC GCGTTTCGC TCGGGCGGGG
PMC21	GCAACGGTAA AAATATCGAC ATGCCACTT CGATGACCCC GCAATTTC GCGTTTCGC TCGGGCGGGG
EG327	GCAACGGCAA AAATATCGAC ATGCCACTT CGATGACCCC GCAATTTC GCGTTTCGC TCGGGCGGGG
Consensus	<u>GCAACGG-AA AAATATCGAC ATGCCACTT CGATG-C-CC GCA-TTTTC GCGTTTCGC TCGG-GCGGG</u>

C5

1401	1470
H15	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
BZ10	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
BZ198	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
P20	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
H38	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
Z2491	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
H41	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
EG329	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
PMC21	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
EG327	GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA
Consensus	<u>GGCGGATGCG CCCACTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTG GCAAGCAAGGA TGCCAACAAA</u>

C5

	1471	1540
H15	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
BZ10	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
BZ198	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
P20	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
H38	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
Z2491	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
H41	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCG CAACTTAAAG	
EG329	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
PMC21	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
EG327	CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG	
Consensus	<u>CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG</u>	
	C5	
	1541	1610
H15	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACCGC CGCGCGGGTA TCGCCAAGC	
BZ10	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACCGC CGCGCGGGTA TCGCCAAGC	
BZ198	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACCGC CGTGCGGGCA TCGCCAAGC	
P20	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGAA CGGCAACCGC CGCGCGGGTA TCGCCAAGC	
H38	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACCGC CGTGCGGGCA TCGCCAAGC	
Z2491	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACCGC CGTGCGGGCA TCGCCAAGC	
H41	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGAA CGGCAACCGC CGTGCGGGCA TCGCCAAGC	
EG329	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACCGC CGTGCGGGCA TCGCCAAGC	
PMC21	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACCGC CGTGCGGGCA TCGCCAAGC	
EG327	GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACCGC CGTGCGGGCA TCGCCAAGC	
Consensus	<u>GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGAA CGGCAACCGC CGTGCGGGCA TCGCCAAGC</u>	
	C5	
	1611	1680
H15	GATTGCAACC GCAGGTTTGG CTCAGGGTA TTTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGTACT	
BZ10	GATTGCAACC GCAGGTTTGG CTCAGGGTA TTTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGTACT	
BZ198	GATTGCAACC GCAGGTCTAG TTCAGGGTA TCTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGACACT	
P20	GATTGCAACC GCAGGTTTGG CTCAGGGTA TTTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGTACT	
H38	GATTGCAACC GCAGGTCTGG TTCAGGGTA TCTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGGCACT	
Z2491	GATTGCAACC GCAGGTCTGG TTCAGGGTA TCTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGGCACT	
H41	GATTGCAACC GCAGGTCTGG TTCAGGGTA TCTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGGCACT	
EG329	GATTGCAACC GCAGGTCTGG TTCAGGGTA TTTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGGCACT	
PMC21	GATTGCAACC GCAGGTCTGG TTCAGGGTA TTTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGGCACT	
EG327	GATTGCAACC GCAGGTCTGG TTCAGGGTA TCTGCCCGC AAGAGTATGA TGGCGATCGG CGGCGGGCACT	
Consensus	<u>GATTGCAACC GCAGGT-T-G -TCAGGC-TA T-TGCCCGC AAGAGTATGA TGGCGATCGG CGGCG--ACT</u>	
	C5	

FIG. 2

Y D E Y C G A G G T C G G G C G

	1681	1750	1815
H15	TATCGGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
BZ10	TATCGGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
BZ198	TATCGGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
P20	TATCTGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
H38	TATCGGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
Z2491	TATCGGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
H41	TATCTGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
EG329	TATCGGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
PMC21	TATCGGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
EG327	TATCGGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAGG		
Consensus	TATC-CGGCG AAGCCGGTTA -GCCATCGGC TACTCG-A TTTC-G-C-- GG-AAATTGG -TTATCAA-G		
	C5		
			C5
H15	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
BZ10	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
BZ198	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
P20	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
H38	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
Z2491	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
H41	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
EG329	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
PMC21	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
EG327	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		
Consensus	GCACGGCTTC CGGGAAATTTC CGGGGCCATT TCGGTGCTTC CGCATCTGTC GTTATCAGT GTAA		

FIG. 2

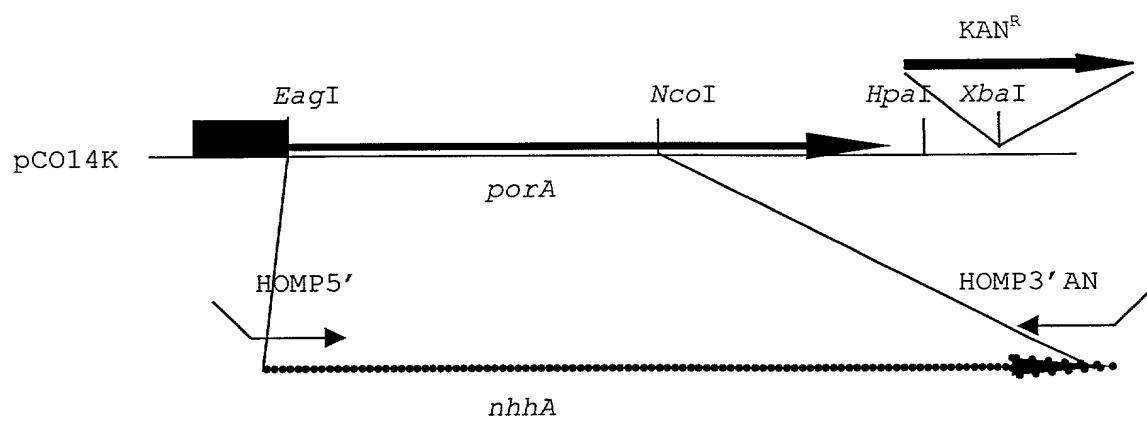
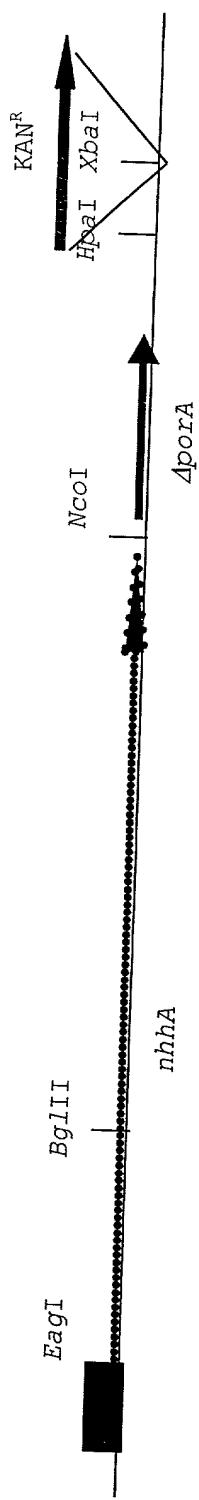
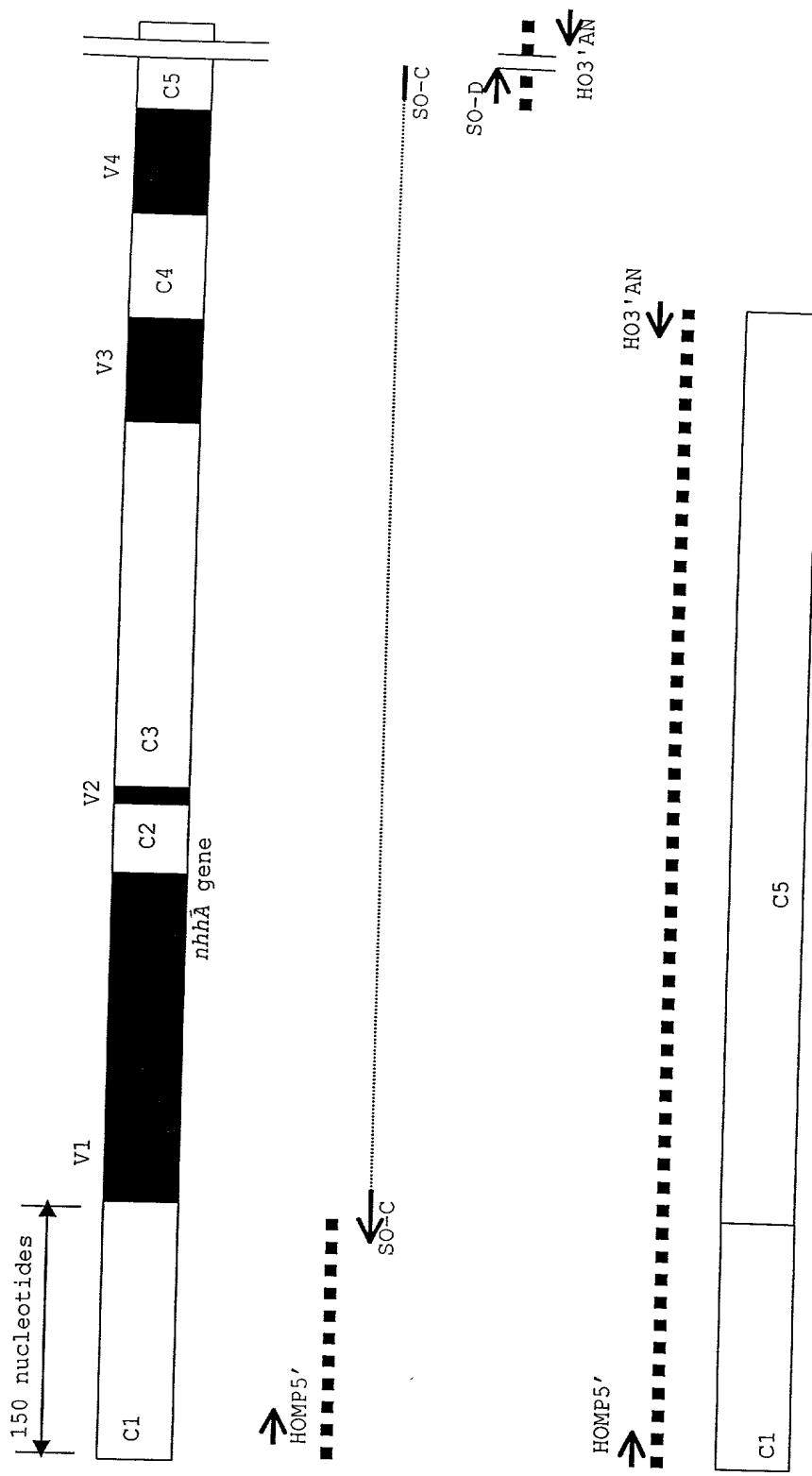
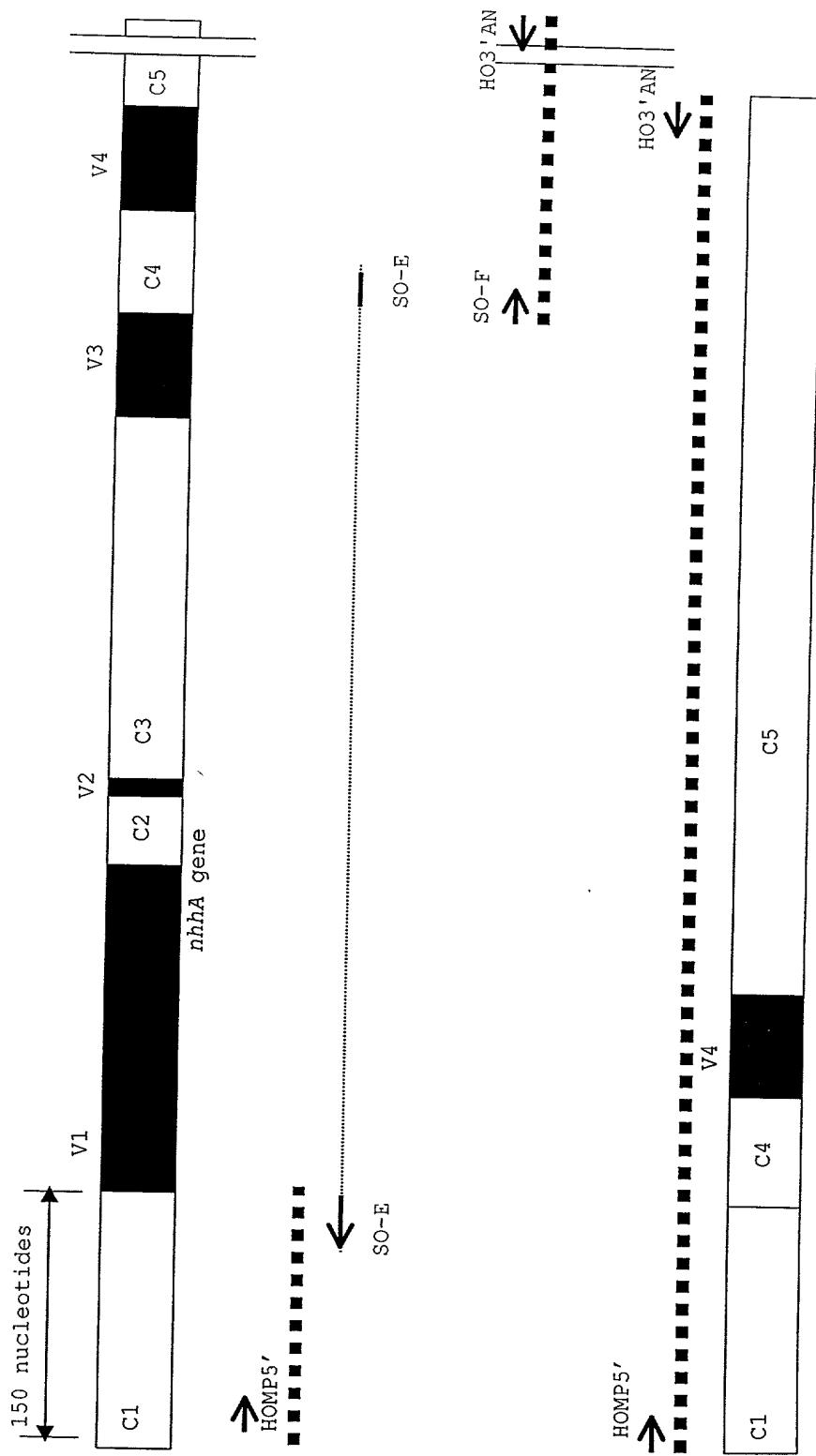


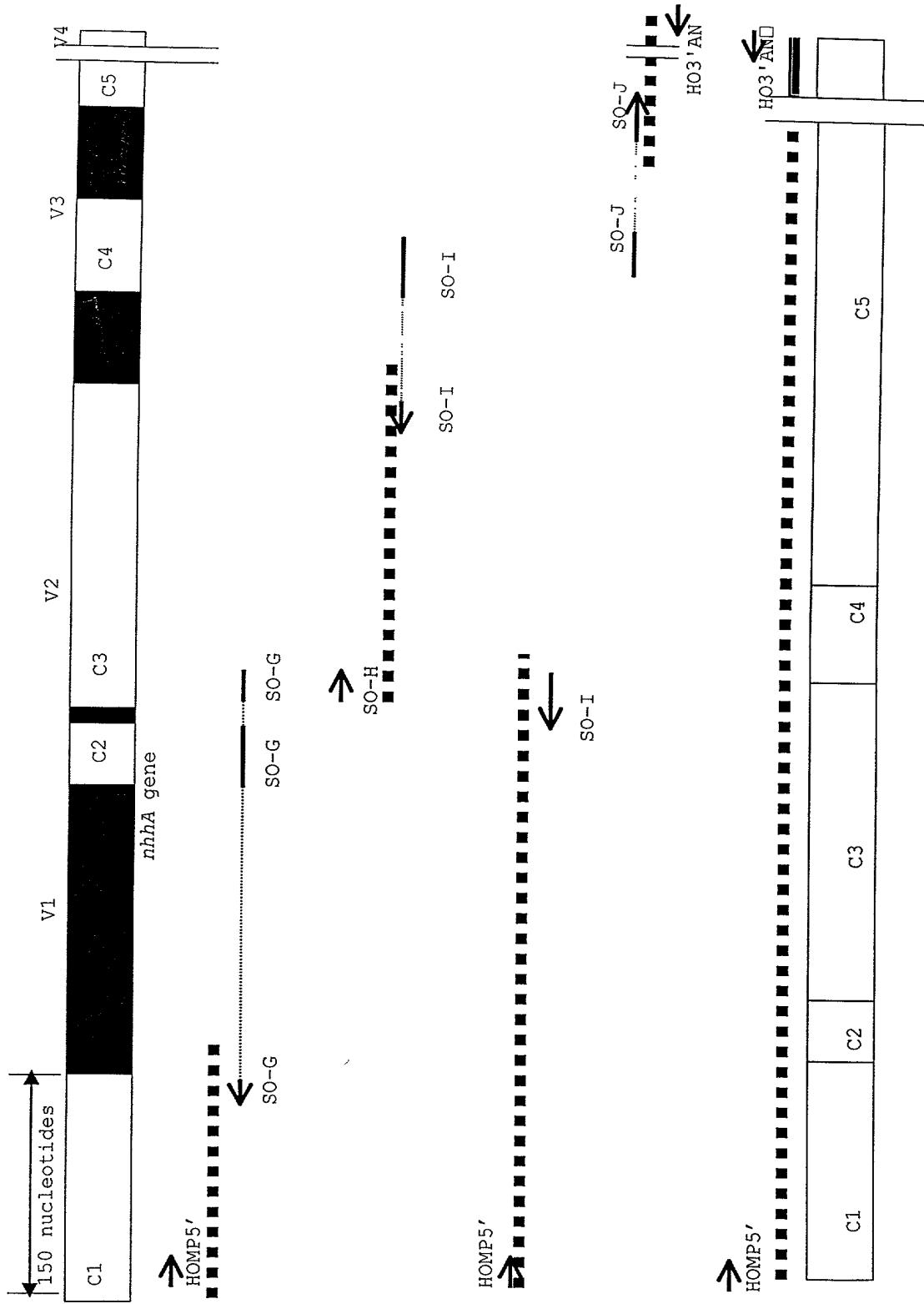
FIG. 3A

pIP52 (PMC21)

**FIG. 3B**

**FIG. 4A**

**FIG. 4B**

**FIG. 4C**

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANNETDLTSV GTEKLSFSAN GNKVNITSDE KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLTDI LLNTGATTNV TDNDVTDDEK KRAASVKDVL NAGWNIKGVK
 151 PGTASDNVD FVRTYDTVEF LSADTKTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEKDGLV TGDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTIA
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLDISKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG
 451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGHNII KGTASGNSRG
 501 HFGASASVGY QW*

FIG. 5A

1 ATGAACAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAAATG AAACAGATCT GACCAGTGTG GGAACGTAAA ATTATCGTT
 201 TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA
 251 ATTTTGCAGA AGAAACGGCT GGGACGAACG GCGACACCCAC GTTCACTCTG
 301 AACGGTATTG GTTCGACTTT GACCGATACG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AACACGTGC
 401 CAAGCGTTAA AGACGTATTA AACGCTGGCT GGAACATTAA AGGCCTTAAA
 451 CCCGGTACAA CAGCTCCGA TAACGTTGAT TTCGTCCGCA CTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAGACGG TAAGTTGGTT ACTGGTAAAG ACAAAAGGCGA
 651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAAGAAG
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAACCGCT
 751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTATGTATG ATGTAATGT CGGCGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAATTGG ATTCAAAGC
 951 GTTGCAGGT TCTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
 1051 ATTACCCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 GTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTGAGCG
 1151 TGGATGGGGA CGCATTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC
 1201 CGCATTACCA ATGTCGCCCG GGGCGTTAAA GAGGGGGATG TTACAAACGT
 1251 CGCACAACTT AAAGGCGTGG CGCAAAACTT GAACAAACCGC ATCGACAATG
 1301 TGGACGGCAA CGCGCGTGC GGCATCGCCC AAGCGATTGC AACCGCAGGT
 1351 CTGGTTCAAGG CGTATTGCG CCGCAAGAGT ATGATGGCGA TCGGCAGCG
 1401 CACTTATCGC GGCAGGCCG GTTACGCCAT CGGCTACTCC AGTATTCCG
 1451 ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGC
 1501 CATTTCGGTG CTTCCGACATC TGTCGGTTAT CAGTGGTAA

FIG. 5B

1 MNKIYRIIWN SALNAWAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 51 ATDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLTDN LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEKDGGKLV TGKGKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTAA
 251 NGQTGQADKF ETVTSGTKVT FASGNGTAT VSKDDQGNIT VKYDVNVGDA
 301 LNVNQLQNSG WNLDISKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE
 351 ITRNGKNIDI ATSMTPOFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
 451 GLVQAYLPKG SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNR
 501 GHFGASASVG YQW*

FIG. 6A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT
 51 CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACACCTGTT TTGCAACGGT TCAGGCGAAT
 151 GCTACCGATG AAACAGGGCT GATCAATGTT GAAACTGAAA ATTATCGTT
 201 TGGCGAACAC GGCAAGAAAG TCAACATCAT AAGCGACACC AAAGGCTTGA
 251 ATTCGCGAA AGAAACGGCT GGGACGAACG GCGACACCC GGTTCATCTG
 301 AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACAGTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTA AACCGAGGCT GGAACATTAAGGCGTTAAA
 451 CCCGGTACAA CAGCTCCGA TAACGTTGAT TTCGTCGGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCAG
 651 GAATGGTTCT TCTACAGACG AAGGCAGGCT CTTAGTGACT GCAAAGAAG
 701 TGATTGATGC AGTAAACAAAG GCTGGTTGGA GAATGAAAAC AACAAACCGCT
 751 AATGGTCAAAG CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAAAGTAACC TTTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAATGTT CGCGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAATTGG ATTCCAAAGC
 951 GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTAA ATGCCGGCAA CAACATCGAG
 1051 ATTACCCGCA ACGGCAAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 ATTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTAAGCG
 1151 TGGATGACGA GGGCGCGTTG AATGTCGGCA GCAAGGATGC CAACAAACCC
 1201 GTCCGCATTA CCAATGTCGC CCCGGCGTT AAAGAGGGGG ATGTTACAAA
 1251 CGTCGCGCAA CTTAAAGGTG TGGCGCAAAA CTTGAACAAAC CGCATCGACA
 1301 ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA
 1351 GGTCTGGTTC AGGCCTATCT GCCCCGGCAAG AGTATGATGG CGATCGGC
 1401 CGGCACATTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATTT
 1451 CGGCCGGCGG AAATTGGATT ATCAAAGGCA CGGCTCCGG CAATTGCGC
 1501 GGCCATTTCG GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA

FIG. 6B

1 MNKIYRIIWN SALNAVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
 101 DGKLVTGKDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
 151 QADKFETVTS GTNVTFAASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
 201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
 301 APGVKEGDVTI NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLIVQAY
 351 LPGKSMMAI GGTYRGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
 401 ASVGYQW*

FIG. 7A

1 ATGAACAAAA TATAACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAAACG TTGATTTCGT CCGCACTTAC GACACAGTCG AGTTCTTGAG
 201 CGCAGATAACG AAAACAACGA CTGTTAATGT GGAAAGCAAA GACAACGGCA
 251 AGAAAACCGA AGTTAAAATC GGTGCGAAGA CTTCTGTTAT TAAAGAAAAAA
 301 GACGGTAAGT TGGTTACTGG TAAAGACAAA GGCAGAATG GTTCTTCTAC
 351 AGACGAAGGC GAAGGCTTAG TGACTGCAAAGAAGTGATT GATGCAGTAA
 401 ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAAACAGGT
 451 CAAGCTGACA AGTTTGAAC CGTTACATCA GGCACAAATG TAACCTTTGC
 501 TAGTGGTAAA GGTACAACTG CGACTGTAAG TAAAGATGAT CAAGGCAACA
 551 TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAAA CGTCAATCAG
 601 CTGAAAACA GCGGTTGGAA TTGGGATTCC AAAGCGGTTG CAGGTTCTTC
 651 GGGCAAAGTC ATCAGCGGC ATGTTTCGCC GAGCAAGGGAA AAGATGGATG
 701 AAACCGTCAA CATTAAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT
 751 AAAAATATCG ACATGCCAC TTCGATGACCC CGCGAGTTTT CCACCGTTTC
 801 GCTCGGGCGCG GGGGCGGAT CGCCCACCTT GAGCGTGGAT GGGGACGCAT
 851 TGAATGTCGG CAGCAAGAAG GACAACAAAC CGTCGGCAT TACCAATGTC
 901 GCCCCGGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG
 951 CGTGGCGCAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCGC
 1001 GTGCGGGCAT CGCCCAAGCG ATTGCAACCG CAGGCTGGT TCAGGCGTAT
 1051 TTGCCCCGGCA AGAGTATGAT GGCGATCGGC GGCGGACTT ATCGCGGGCGA
 1101 AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTGGA
 1151 TTATCAAAGG CACGGCTTCC GGCAATTCCGC CGGGCATTG CGGTGCTTCC
 1201 GCATCTGTCG GTTATCAGTG GTAA

FIG. 7B

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKAVLA TLLFATVQAS
 51 ANRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
 101 VNVESKDNKG KTEVKIGAKT SVIKEKDGL VTGKDKGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTTT ANGQTGQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQGNVI TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN
 251 VSPSKGMDE TVNINAGNNI EITRNGKNID IATSMPQFS SVSLGAGADA
 301 PTLSVDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
 351 RIDNDGNAR AGIAQAIATA GLVQAYLPGK SMMAIGGGTY RGEAGYAIGY
 401 SSISDGNNWI IKGTASGNR GHFGASASVG YQW*

FIG. 8A

1 ATGAACAAAA TATAACCGCAT CATTGGAAT AGTGCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACCGGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACCGTG CGGCAAGCGT TAAAGACGTA TTAAACGCTG GCTGGAACAT
 201 TAAAGGCCTT AAACCCGGTA CAAACAGCTTC CGATAACGTT GATTTCGTCC
 251 GCACTTACGA CACAGTCGAG TTCTTGAGCG CAGATACGAA ACAAACGACT
 301 GTTAATGTGG AAAGCAAAGA CAACGGCAAG AAAACCGAAG TTAAAATCGG
 351 TGCAGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 401 AAGACAAAGG CGAGAAATGGT TCTTCTACAG ACGAAGGCAG AGGCTTAGTG
 451 ACTGCAAAGG AAGTGATTGA TGCAGTAAAC AAGGCTGGTT GGAGAATGAA
 501 AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG TTTGAAACCG
 551 TTACATCAGG CACAAATGTA ACCTTGCTA GTGGTAAAGG TACAACGTGCG
 601 ACTGTAAGTA AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA
 651 TGTCGGCGAT GCCCTAAACG TCAATCAGCT GCAAAACAGC GGGTGGAAATT
 701 TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
 751 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG
 801 CAACAAACATC GAGATTACCC GCAACGGTAA AAATATCGAC ATGCCACTT
 851 CGATGACCCC GCAGTTTCC AGCGTTTCGC TCGGCGGGGG GGGGGATGCC
 901 CCCACTTGA GCGTGGATGG GGACGCATTG AATGTCGGCA GCAAGAAGGA
 951 CAACAAACCC GTCCGCATTA CCAATGTCGC CCCGGGGTT AAAGAGGGGG
 1001 ATGTTACAAA CGTCGCACAA CTAAAGGCG TGGCGAAAA CTTGAACAAAC
 1051 CGCATCGACA ATGTGGACGG CAACCGCGT GCAGGGCATCG CCCAAGCGAT
 1101 TGCAACCGCA GGTCTGGTTC AGGCCTATT GCCCCGGCAAG AGTATGATGG
 1151 CGATCGGCAGG CGGCACTTAT CGCGGCAGG CGGGTTACGC CATCGGCTAC
 1201 TCCAGTATTG CCGACGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG
 1251 CAATTGCGC GGCCATTTCG GTGCTTCCGC ATCTGTCGGT TATCAGTGGT
 1301 AA

FIG. 8B

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK
 101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLMAG WNIKGVKNVD
 151 FVRTYDTVEF LSADTKTTV NVESKDNGKK TEVKIGAKTS VIKEKDGLV
 201 TGDKDGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTAA NGQTQADKF
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
 301 WLDSKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE ITRNGKNIDI
 351 ATSMTPQFSS VSLGAGADAP TLSVGDALN VGSKKDNKPV RITNVAPGVK
 401 EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNNSRG HFGASASVGY
 501 QW*

FIG. 9A

1 ATGAACAAAAA TATAACCGCAT CATTGGAAT AGTGCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACCGGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AATTACACCTA
 201 CTCGCTGAAA AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT
 251 TATCGTTAG CGCAAACGGC AATAAAGTC ACATCACAAG CGACACCAAA
 301 GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 351 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATCGTGC GCAAGCGTTA
 401 AAGACGTATT AAACGCTGGC TGBAACATTAA AAGGCCTTAA AACACGTTGAT
 451 TTCGTCCGCA CTTACGACAC AGTCGAGTTC TTGAGCGCAG ATACGAAAAC
 501 AACGACTGTT AATGTGGAAA GCAAAGACAA CGGCAAGAAA ACCGAAGTTA
 551 AAATCGGTGC GAAGACTTCT GTTATTAAAG AAAAAGACGG TAAGTTGGTT
 601 ACTGGTAAAG ACAAAAGCGA GAATGGTTCT TCTACAGACG AAGGCAGAAGG
 651 CTTAGTGACT GCAAAAGAAG TGATTGATGC AGTAAACAAAG GCTGGTTGGA
 701 GAATGAAAAC ACAACCCGCT AATGGTCAAA CAGGTCAAGC TGACAAGTTT
 751 GAAACCGTTA CATCAGGCAC AAATGTAACC TTTGCTAGTG GTAAAGGTAC
 801 AACTGCGACT GTAAGTAAAG ATGATCAAGG CAACATCACT GTATGTATG
 851 ATGAAATGTC CGGCGATGCC CTAACACGTCA ATCAGCTGCA AAACAGCGGT
 901 TGGAAATTGG ATTCCAAAGC GGTGCAAGGT TCTTCGGGCA AAGTCATCAG
 951 CGGCAATGTT TCGCCGAGCA AGGGAAAGAT GGATGAAACC GTCAACATTA
 1001 ATGCCGGCAA CAACATCGAG ATTACCCGCA ACGGTAAGAA TATCGACATC
 1051 GCCACTTCGA TGACCCCGCA GTTTCCAGC GTTCGCTCG GCGCGGGGGC
 1101 GGATGCGCCC ACTTTGAGCG TGATGGGGA CGCATTGAAT GTCGGCAGCA
 1151 AGAAGGACAA CAAACCCGTC CGCATTACCA ATGTCGCCCC GGGCGTTAAA
 1201 GAGGGGGATG TTACAAACGT CGCACAACTT AAAGGCCTGG CGCAAAACTT
 1251 GAACAACCGC ATCGACAATG TGACGGCAA CGCGCGTGC GGCATCGCCC
 1301 AAGCGATTGC AACCGCAGGT CTGGTTCAAGG CGTATTGCC CGGCAAGAGT
 1351 ATGATGGCGA TCGCCGGCGG CACTTATCGC GGCAGAGCCG GTTACGCCAT
 1401 CGGCTACTCC AGTATTCCG ACGGCAGAAA TTGGATTATC AAAGGCACGG
 1451 CTTCCGGCAA TTCGCGCGGC CATTTCGGTG CTTCCGCATC TGTCGGTTAT
 1501 CAGTGGTAA

FIG. 9B

H41 PMC21 H41Stude1 PMC21Bglde1 PMC21C1C5	1 <u>MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN</u> <u>MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATVNNTAVLA TLLFATVQAS</u> <u>MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN</u> <u>MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS</u> <u>MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS</u> C1	50
H41 PMC21 H41Stude1 PMC21Bglde1 PMC21C1C5	51 <u>ATDED..EEE ELESVQRS.V VGSIQASMEG SVELET...I SLSMTNDSKE</u> <u>ANNEEQEEYI YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK</u> ATDE ANNE AN	100
	V1	
H41 PMC21 H41Stude1 PMC21Bglde1 PMC21C1C5	101 <u>FVDPYIVVTL KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK</u> <u>GVLTAREITL KAGDNLKIKO NGTN..... FTYSLKKDL TDLTSGTEK</u> V1	150
	C2	V2
	C3	
H41 PMC21 H41Stude1 PMC21Bglde1 PMC21C1C5	151 <u>LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT</u> <u>LSFSAHGNKV NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT</u> <u>LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT</u> <u>LSFSANGNKV NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT</u> C3	200
		V3
H41 PMC21 H41Stude1 PMC21Bglde1 PMC21C1C5	201 <u>GATTNVNTNDN VTDDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDVFVRT</u> <u>GATTNVNTNDN VTDDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDVFVRT</u> <u>GATTNVNTNDN VTDDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDVFVRT</u> <u>GATTNVNTNDN VTDDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDVFVRT</u> V3	250
	C4	V4
	C5	
H41 PMC21 H41Stude1 PMC21Bglde1 PMC21C1C5	251 <u>YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKG</u> <u>YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD</u> <u>YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKG</u> <u>YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD</u> <u>YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD</u> C5	300
H41 PMC21 H41Stude1 PMC21Bglde1 PMC21C1C5	301 <u>KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT QOADKFETVT</u> <u>KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT QOADKFETVT</u> <u>KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT QOADKFETVT</u> <u>KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT QOADKFETVT</u> <u>KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT QOADKFETVT</u> C5	350
H41 PMC21 H41Stude1 PMC21Bglde1 PMC21C1C5	351 <u>SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVDALNVN OLONSGWNLD</u> <u>SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVDALNVN OLONSGWNLD</u> <u>SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVDALNVN QLONSGWNLD</u> <u>SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVDALNVN QLONSGWNLD</u> <u>SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVDALNVN QLONSGWNLD</u> C5	400

FIG. 10

	401		450
H41	<u>SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM</u>		
PMC21	<u>SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM</u>		
H41Studel	SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM		
PMC21Bgldel	SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM		
PMC21C1C5	SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM		
	C5		
	451		500
H41	<u>TPQFSSVSLG AGADAPTLSV DDEGALNVGS KDANKPVRIT NVAPGVKEGD</u>		
PMC21	<u>TPQFSSVSLG AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD</u>		
H41Studel	TPQFSSVSLG AGADAPTLSV DDEGALNVGS KDANKPVRIT NVAPGVKEGD		
PMC21Bgldel	TPQFSSVSLG AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD		
PMC21C1C5	TPQFSSVSLG AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD		
	C5		
	501		550
H41	<u>VTNVAOLKGV AONLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA</u>		
PMC21	<u>VTNVAOLKGV AONLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA</u>		
H41Studel	VTNVAQLKGV AONLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA		
PMC21Bgldel	VTNVAQLKGV AONLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA		
PMC21C1C5	VTNVAQLKGV AONLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA		
	C5		
	551		600
H41	<u>IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.</u>		
PMC21	<u>IGGGTYRGEA GYAIGYSSIS DGGNWIIKGT ASGNSRGHFG ASASVGYQW.</u>		
H41Studel	IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.		
PMC21Bgldel	IGGGTYRGEA GYAIGYSSIS DGGNWIIKGT ASGNSRGHFG ASASVGYQW.		
PMC21C1C5	IGGGTYRGEA GYAIGYSSIS DGGNWIIKGT ASGNSRGHFG ASASVGYQW.		
	C5		

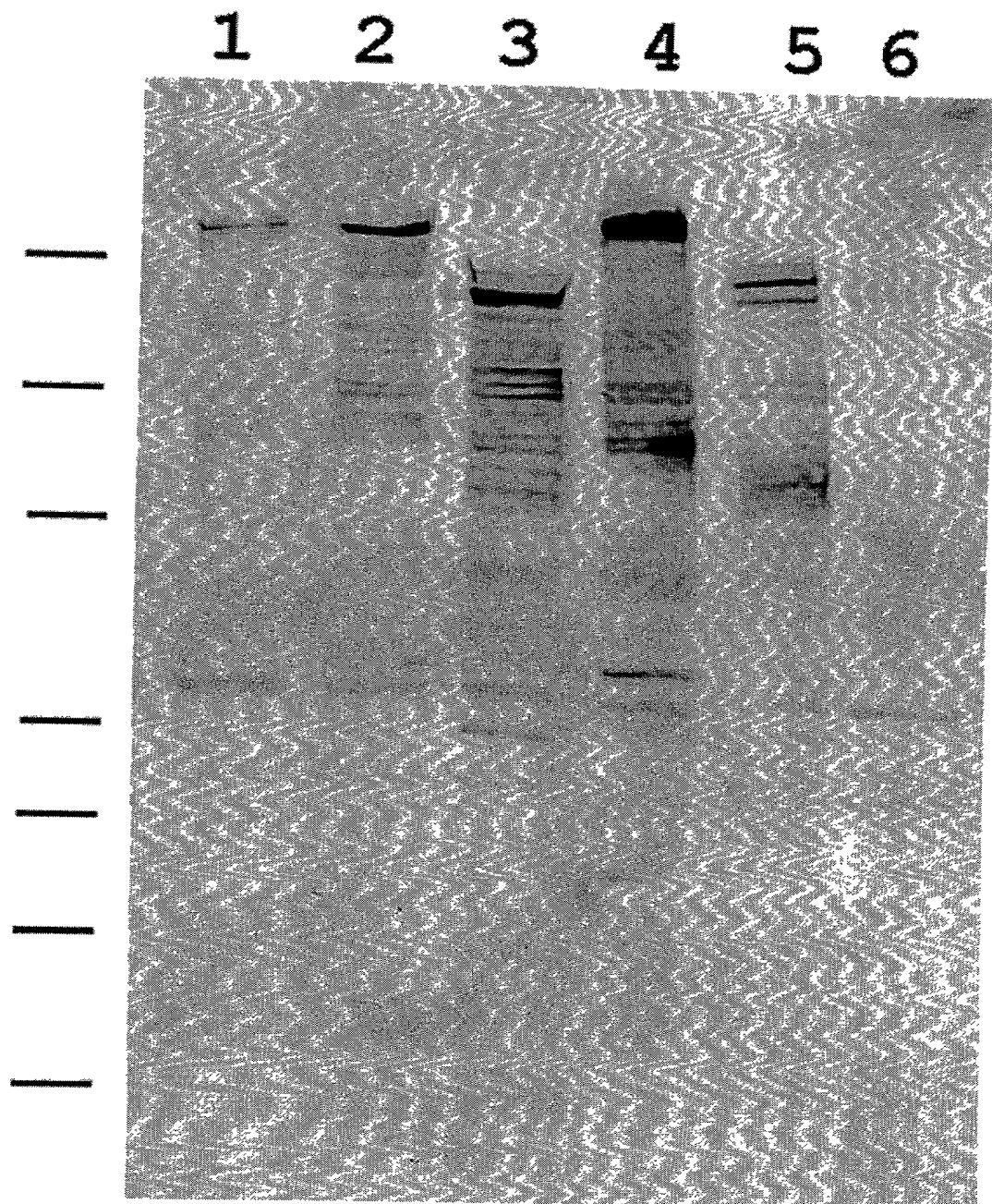


FIG. 11

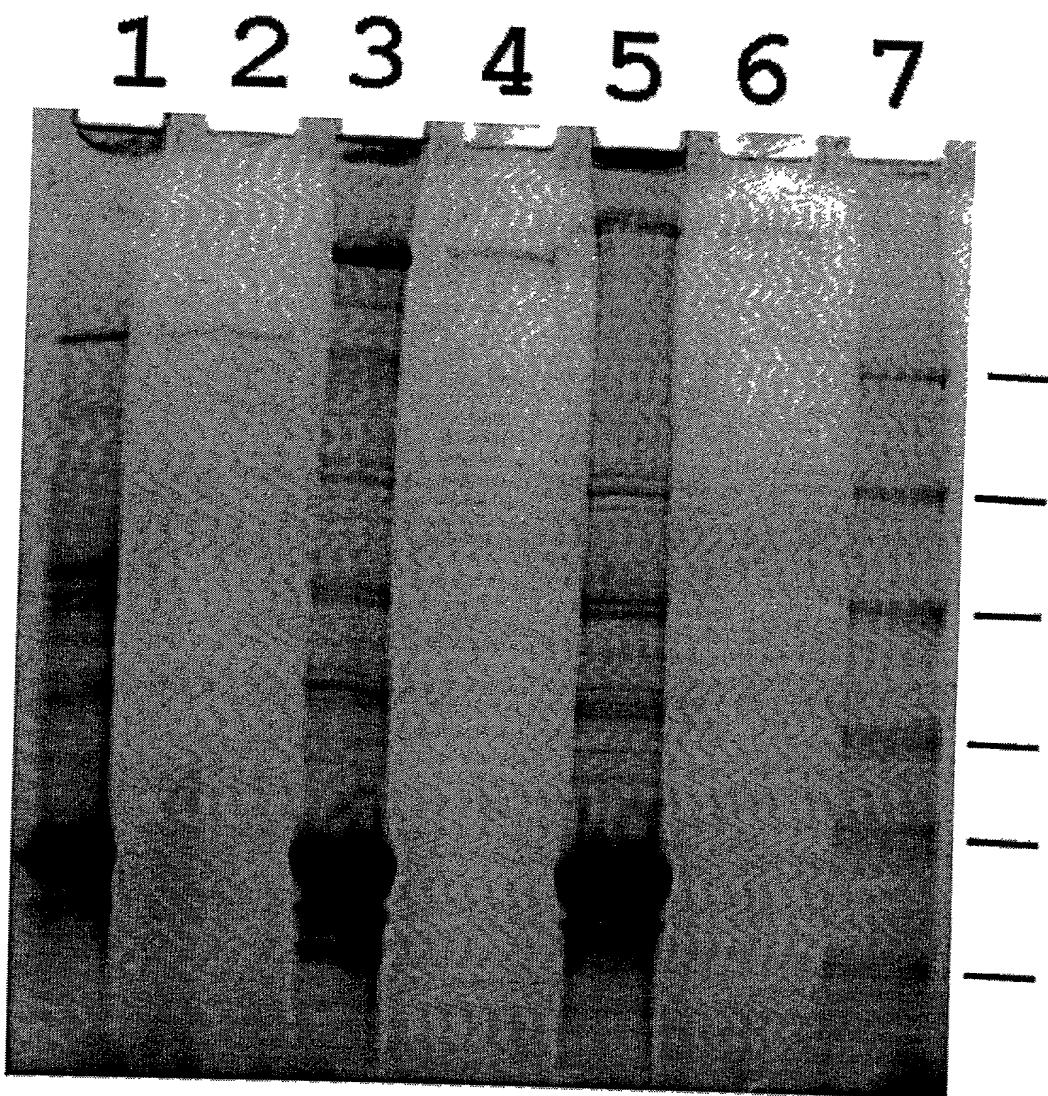
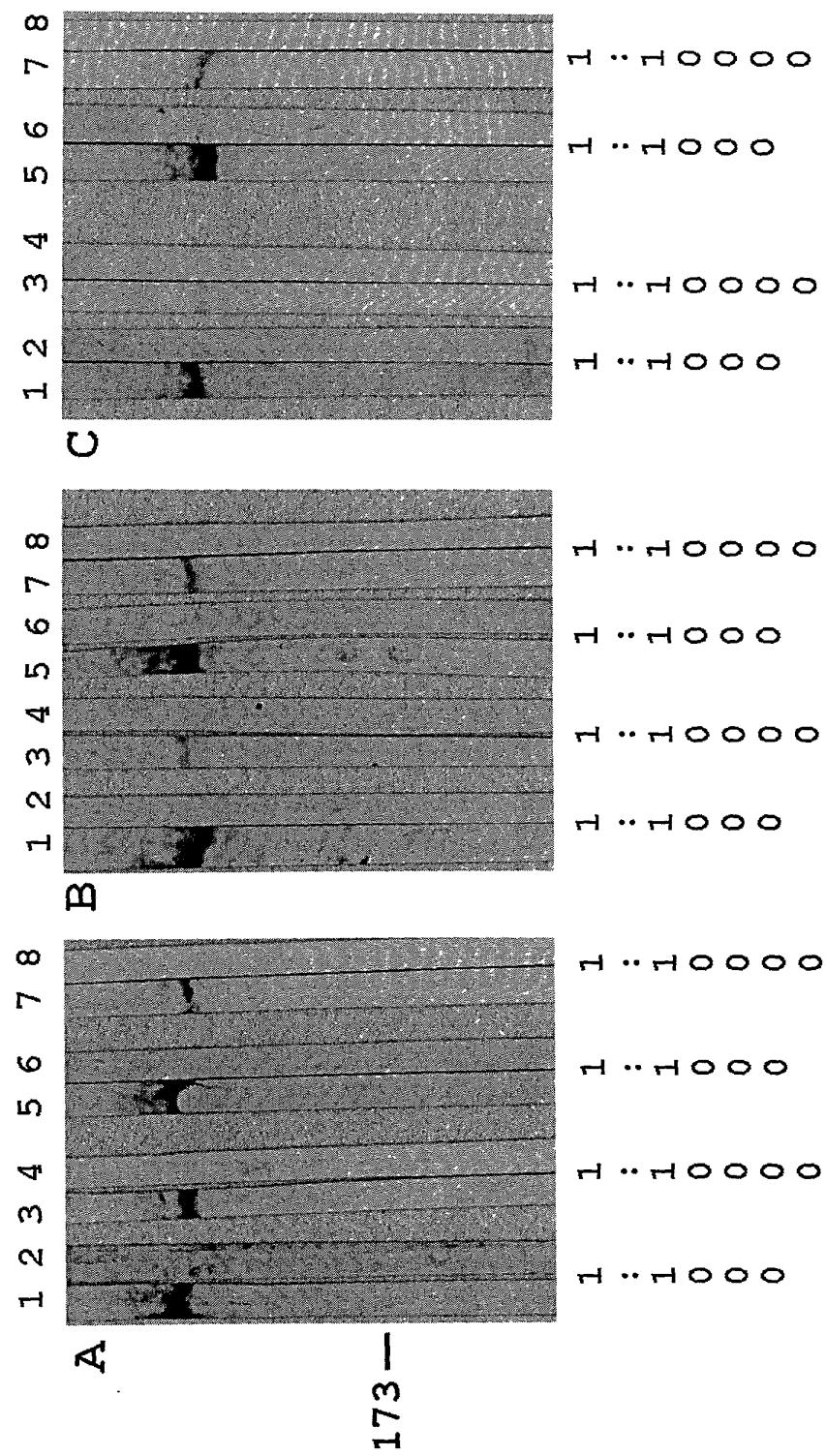


FIG. 12

**FIG. 13**

52 NNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
 101 GVLTAREITL KAGDNLIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG
 151 NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL LNTGATTNVT
 201 NDNVTDDEKK RAASVKDVNL AGWNIKGVKP GTTASDNVDF VRTYDTVEFL
 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
 301 TDEGEGLVTA KEVIDAVNKA GWRMKTTAN GQTGQADKFE TVTSGTNVTF
 351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
 401 SGKVISGNVS PSKGKMDETV NINAGNNIEI TRNGKNIDIA TSMPQFSSV
 451 SLGAGADAPT LSVDGDALNV GSKKDNPVPR ITNVAPGVKE GDVTNVAQLK
 501 GVAQNLNNRI DNVDGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG
 551 EAGYAIGYSS ISDGGSNIK GTASGNSRGH FGASASVGYQ W*

FIG. 14A

52 TDEDEEEEL ESVQRSVVGS IQASMEGSVE LETISLSMTN DSKEFVDPYI
 101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTGLINVE TEKLSFGANG
 151 KKVNIIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML LNTGATTNVT
 201 NDNVTDDEKK RAASVKDVNL AGWNIKGVKP GTTASDNVDF VRTYDTVEFL
 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKKGKGENGSS
 301 TDEGEGLVTA KEVIDAVNKA GWRMKTTAN GQTGQADKFE TVTSGTKVTF
 351 ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
 401 SGKVISGNVS PSKGKMDETV NINAGNNIEI TRNGKNIDIA TSMPQFSSV
 451 SLGAGADAPT LSVDDEGALN VGSKDANKPV RITNVAPGVK EGDVTNVAQL
 501 KGVAQNLNNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL
 551 GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVGY QW*

FIG. 14B

52 NNETDLTSV GTEKLSFSAN GNKVNITSDT KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLTD~~T~~ LLNTGATTNV TNDNVT~~D~~DEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEKD~~G~~KLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT~~TA~~
 251 NGQTGQADKF ETVTSGTNVT FASGKGT~~T~~TAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLD~~S~~KAVAG SSGKVISGNV SPSKGKMD~~E~~T VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG
 451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
 501 HFGASASVGY QW*

FIG. 14C

52 TDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLDM LLNTGATTNV TNDNVT~~D~~DEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEKD~~G~~KLV TGKGKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT~~TA~~
 251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
 301 LNVNQLQNSG WNLD~~S~~KAVAG SSGKVISGNV SPSKGKMD~~E~~T VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVD~~E~~GAL NVGSKDANKP
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
 451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
 501 GHFGASASVG YQW*

FIG. 14D

52 NNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
 101 DGKLVTGKDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
 201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
 351 LPGKSMMMAIG GGTYRGEAGY AIGYSSISDG GNWIWIKGTAS GNSRGHFGAS
 401 ASVGYQW*

FIG. 14E

PROTEIN: 23871 C/60

52 NRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGL VTKDKGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTTT ANGQTGQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQGNI TVMYDVGND ALNVNQLQNS GWNLDLSKAVA GSSGKVISGN
 251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
 301 PTLSVDGDAL NVGSKKDNP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPGK SMMAIGGGTY RGEAGYAIGY
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*

FIG. 14F

50 SANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK
 101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD
 151 FVRTYDTVEF LSADTKTTV NVESKDNGKK TEVKIGAKTS VIKEKDGLV
 201 TGDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTA NGQTGQADKF
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVGDA LNQNQLQNSG
 301 WNLDLSKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE ITRNGKNIDI
 351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
 401 EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY
 501 QW*

FIG. 14G